A Curve for all Reasons

The Rectangular Hyperbola in Biology

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The cause-effect relationship for a wide variety of biological processes from molecular to ecosystem levels can be described by a curvilinear function called the rectangular hyperbola. Although a simple algebraic equation adequately describes this curve, biological models have generated different equations incorporating biologically meaningful parameters. The Michelis–Menten equation describing enzyme kinetics, and the Type II functional response of predators to changing prey densities are two such examples.

To a keen observer, nature reveals an infinite variety of fascinating patterns everywhere – in snowflakes, beehives, zebra's stripes and branching trees. If the observer happens to be a trained biologist, he might ask – 'what is the mechanism that produces this pattern and what is its significance?' A mathematician, on the other hand, might start wondering if the observed pattern obeys any mathematical rule, or whether it could be described by some equation. Some mathematicians, who draw inspiration from biology, feel that every pattern in the living world, ranging from the folding of a hemoglobin molecule to the growth of tropical forests can be described in mathematical terms. An ever-increasing number of biologists, even if they do not share this extreme view, are beginning to realize that a mathematical approach could help in gaining insights into the mechanisms underlying many biological systems.

There was a time when population genetics and population ecology were considered to be the only areas of biology that lent themselves to mathematical reasoning or modelling, but not any more. Other areas of biology, notably various branches of ecology, ethology, taxonomy and molecular biology have also been enriched in recent years by mathematical approaches.

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Unfortunately, biological systems are extremely complex, and our knowledge about the laws governing their components is often not detailed enough to allow us to write down an appropriate equation describing each component. Nevertheless, it is usually possible for us to reduce the complexity of many biological systems by making a series of simplifying assumptions which allow us to replace the real system with an imaginary model system; if our assumptions are reasonable and realistic, the model will then be applicable to the real biological system.

The cause-effect relationship in any branch of science may be stated algebraically as $Y = f(X)$ (i.e. Y is a function of X), and when shown graphically, results in a 'curve' that can be described with an appropriate equation. Among such curves (Gaussian, sigmoid, hyperbolic, exponential, etc.) the rectangular hyperbola, also called saturating hyperbola, decelerating curve or asymptotic regression is probably the most ubiquitous curve in biology (see *Box* 1). An amazing variety of phenomena at different levels of biological organization, ranging from reaction velocity of enzymes to stability of ecosystems are found to be adequately described by the rectangular hyperbola (*Table* 1).

Box 1. Rectangular Hyperbola
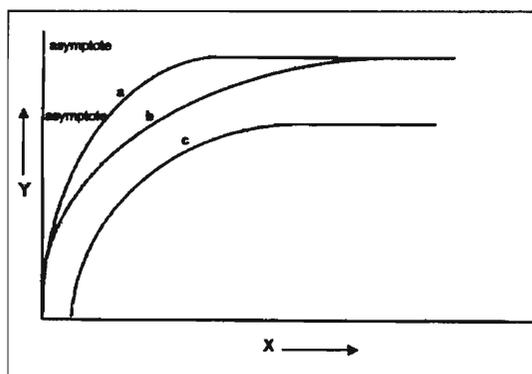
The rectangular hyperbola is described by the following equation:

$$Y = (1 - e^{-aX}), \quad \text{where}$$

Y is the dependent variable, X is the independent variable, and a is a parameter to be estimated.

Using this equation, one can proceed with simple curve fitting, without having to know what parameters X and Y stand for. The curve has two quantifiable attributes – the height of the asymptote and the rate at which it is reached. Curves a and b reach the same aymptote but at different rates, while curves b and c have the same rate of increase but reach different asymptotes. If these attributes for two or more curves have to be compared statistically, the curves are generally linearized first by using empirical logistic regression or by using angularly transformed Y values.

Area	Process	Independent variable (X)	Dependent variable (Y)
Biochemistry	Enzyme kinetics	Substrate concentration	Reaction velocity
Pharmacology	Effect of drugs	Drug concentration	Percent of maximum effect
Physiology	Photosynthesis	Light intensity	Photosynthetic rate
	Algal growth	Nutrient level	Growth rate
Endocrinology	Hormone binding receptors	Hormone dose	Receptor-bound hormone level
Population Ecology	Predator's functional response	Prey density	No. of prey killed
	Optimal offspring size	Offspring size	Offspring fitness
	Optimal foraging time	Foraging time	Net average energy gain
Community Ecology	Species richness	Area sampled	Species richness
	Community stability	Species richness	Degree of resistance to disturbance
	Biodiversity	Potential evapotranspiration	Mammalian species diversity
Applied Ecology	Fish production	Fishing effort	Yield

Biological Models

A simple mathematical model is no more than an appropriate equation that helps us in curve fitting. But once the variables X and Y are identified as some biological parameters, a mere mathematical equation may not satisfy our curiosity. We might, for instance, wish to find out the underlying biological factors that influence the height of the asymptote or the steepness of the curve. Mere curve fitting approaches are inadequate to distinguish minor, but biologically meaningful differences in the shapes of the curves.

Using three examples, one from biochemistry and two from ecology, I illustrate here how biological models, unlike the plain

Table 1. The rectangular hyperbolic function: Examples from different areas of biology with the corresponding independent and dependent variables .

mathematical models, generate equations for the rectangular hyperbola by incorporating important underlying mechanisms. Needless to say, a broad understanding of the basic processes and plausible hypotheses about the underlying mechanisms is a *sine qua non* for developing realistic biological models. The examples I have chosen are:

1. Enzyme reaction velocity as a function of substrate concentration.
2. Offspring fitness as a function of maternal investment.
3. The Type II functional response of a predator to changing prey density.

The relation between enzyme reaction velocity and substrate concentration is described by the celebrated Michaelis–Menten equation[1].

$$V = \frac{V_{max}(S)}{K_m + (S)}$$

where V=velocity of reaction, V_{max}=maximum velocity achieved, S = substrate concentration, K_m = Michaelis–Menten constant.

Enzyme velocity increases with increasing substrate concentration at a decelerating rate, reaching the asymptotic V_{max}. The enzyme is fully saturated at this point and any further increase in substrate concentration has no effect on the enzyme velocity. In this equation, K_m is simply the substrate concentration at which $V = V_{max}/2$. A double reciprocal plot ($1/V$ as a function of $1/(S)$) (called the Lineweaver–Burk plot) linearizes the hyperbolic curve. The Michaelis–Menten equation does not require any additional parameters to be estimated or measured for incorporation into the equation. However, it is certainly an improvement over the purely curve fitting equation in that K_m is considered to be a parameter of considerable significance in enzyme kinetics.

Smith and Fretwell's model of offspring fitness (*f*) as a function

of maternal investment (x), measured as offspring size or biomass, is a typical rectangular hyperbola. Given a fixed quantum of energy available for reproduction during a breeding period, two alternative strategies for a female are production of either a large number of small offspring, or a small number of large offspring. Offspring that are larger at birth can generally be expected to be more likely to survive and have a higher reproductive success later in life. Increasing maternal investment in an individual offspring may, therefore, lead to greater fitness, but only to some extent, because any further investment can be done only at the expense of clutch size. This model can be described by the following equation:

$$f = f_m [1 - e^{-k(x-x_0)}]$$

where f_m = maximum fitness level, k = rate of increase in fitness with increasing offspring size and x_0 = minimum viable offspring size at birth. Note that in this model the curve origin is not at $x = 0$, but at x_0, which is the minimum size at birth that will permit offspring survival, a biological parameter the value of which has to be known. The rate of increase in fitness, k, with offspring size may also have to be estimated based on empirical studies.

The third example concerns analysis of prey-predator interactions, my own area of research, in which we have studied both vertebrate and invertebrate aquatic predators which feed on zooplankton prey. The Type II functional response is one of the three exhibited by predators in response to changing prey densities. Holling's original 'disk' equation,

$$N_a = \frac{a T_t N_0}{1 + a T_h N_0}$$

where N_a = number of prey killed, N_0 = prey density, a = rate of discovering prey, T_t = time available for prey search, T_h = prey handling time, and Rogers' random predator equation

$$N_a = N_0 \{1 - \exp [- a (T_t - T_h N_0)]\}$$

describe the Type II functional response. Both equations incor-

Suggested Reading

[1] M Begon, J L Harper and C R Townsend, *Ecology, individuals, populations and communities*, 3rd ed. Blackwell Science, Oxford, UK, 1996.

[2] T R Rao, Optimality models for prey-predator interactions, in Narain, POP Kathuria, V K Sharma and Prajneshu (eds.), *Recent advances in agricultural statistics research*, pp. 342-353, Wiley-Interscience, New Delhi, 1991.

[3] D S Riggs, *The mathematical approach to physiological problems, A critical primer*, MIT Press, Cambridge, Mass., USA, 445 pp. 1963.

[4] J Maynard Smith, *Mathematical ideas in biology*, Cambridge University Press, Cambridge, UK, 152 pp, 1968.

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porate two important biological parameters – the predator's rate of discovering prey (a), and prey handling time (T_h). These parameters, in turn, are dependent on other biological factors such as predator's hunger level, prey dispersion patterns, prey size and other predator-deterrent morphological and behavioral traits, most of which are, in principle, quantifiable and can be incorporated into an expanded model. The parameters a and T_h, because of their ecological significance, also figure prominently in many other optimal foraging models.

If we measure a predator's response to prey density using two or more prey species differing in their vulnerability to predation, we can generate a set of hyperbolic curves. Then it is more meaningful if the curves are compared in terms of the two predator parameters a, the encounter rate and T_h, the prey handling time. This is possible only if we have some data for these parameters for the different prey species tested. In the absence of such information, Holling's or Rogers' models cannot be used although it might be possible to compare the functional response curves of different prey species with simple mathematical curve fitting. In one of our own studies we could not determine the attack rates or prey handling times for our test species and had to use Michaelis–Menten model for statistical comparison of different curves. In such a situation, we have no idea of the ecological significance if any, of the Michaelis–Menten constant, K_m. For the Type II response curve, K_m would be simply the prey density at which the number of prey ingested by the predator is half the maximum ingested. Here is an example where the ecological modeler had to sacrifice realism to generality. The realism and predictive ability of a biological model generally improves as more biological parameters are incorporated into it. At the same time, independent knowledge of the magnitude of these parameters can often be difficult to acquire.

There are many mathematical models that are useful in understanding various issues in biology. This brief description of one simple model, hopefully, serves as an example of the applicability of simple functions to diverse biological problems.